44. A method for detecting an insecticidal polypeptide in a biological sample comprising contacting a biological sample suspected of containing said insecticidal polypeptide with an antibody in accordance with any one of claims 41, under conditions effective to allow the formation of immunecomplexes, and detecting the immunecomplexes so formed.

45. A transgenic plant having incorporated into its genome a transgene that encodes a polypeptide comprising the amino sequence of SEQ ID NO:59 or SEQ ID NO:61.

46. The transgenic plant of claim 45, wherein said transgene comprises the nucleic acid sequence of SEQ ID NO:58 or SEQ ID NO:60.

47. Progeny of the plant of claim 45.

48. Seed from the plant of claim 45 or 47.

49. A method of selecting a Cry1 polypeptide having increased insecticidal activity against a Lepidopteran insect comprising mutagenizing a population of polynucleotides to prepare a population of polypeptides encoded by said polynucleotides and testing said population of polypeptides and identifying a polypeptide having one or more modified amino acids in a loop region of domain 1 or in a loop region between domain 1 and domain 2, wherein said polypeptide has increased insecticidal activity against said insects.

50. A method of generating a Cry1 polypeptide having increased insecticidal activity against a Lepidopteran insect comprising the steps of:

(a) identifying in said polypeptide a loop region between adjacent α-helices of domain 1 or between an α-helix of domain 1 and a β strand of domain 2;

(b) mutagenizing said polypeptide in at least one or more amino acids of one or more of said identified loop regions; and

(c) testing said mutagenized polypeptide to identify a polypeptide having increased insecticidal activity against said Lepidopteran insects.

51. A method of mutagenizing a Cry1 polypeptide to increase the insecticidal activity of said polypeptide against a Lepidopteran insect, said method comprising the steps of:

(a) predicting in said polypeptide a contiguous amino acid sequence encoding a loop region between adjacent α-helices of domain 1 or between an α-helix of domain 1 and a β strand of domain 2;

(b) mutagenizing one or more of said amino acid residues in said contiguous amino acid sequence to produce a population of polypeptides having one or more altered loop regions;

(c) testing said population of polypeptides for insecticidal activity against said Lepidopteran insect; and

(d) identifying in said population a polypeptide having increased insecticidal activity against said Lepidopteran insect.

52. The method of claim 51, wherein said modified amino acid sequence comprises a loop region between α helices 1 and 2a, α helices 2b and 3, α helices 3 and 4, α helices 4 and 5, α helices 5 and 6, or α helices 6 and 7 of domain 1, or between α helix 7 of domain 1 and β strand 1 of domain 2.

53. The method of any one of claims 52, wherein said loop region between α helices 1 and 2a comprises an amino acid sequence of from about amino acid 41 to about amino acid 47 of a Cry1 protein; said loop region between α helices 2b and 3 comprises an amino acid sequence of from about amino acid 83 to about amino acid 89 of a Cry1 protein; said loop region between α helices 3 and 4 comprises an amino acid sequence of from about amino acid 118 to about amino acid 124 of a Cry1 protein; said loop region between α helices 4 and 5 comprises an amino acid sequence of from about amino acid 148 to about amino acid 156 of a Cry1 protein; said loop region between α helices 5 and 6 comprises an amino acid sequence of from about amino acid 176 to about amino acid 85 of a Cry1 protein; said loop region between α helices 6 and 7 comprises an amino acid sequence of from about amino acid 217 to about amino acid 222 of a Cry1 protein; and said loop region between α helix 7 of domain 1 and β strand 1 of domain 2 comprises an amino acid sequence of from about amino acid 249 to about amino acid 259 of a Cry1 protein.

54. The method of claim 53, wherein said Cry1 protein is a Cry1A, Cry1B, Cry1C, Cry1D, Cry1E, Cry1F, Cry1G, Cry1H, Cry1I, Cry1J, or a Cry1K crystal protein.

55. The method of claim 54, wherein said Cry1 protein is a Cry1Aa, Cry1Ab, Cry1Ac, Cry1Ad, Cry1Ae, Cry1Ba, Cry1Bb, Cry1Bc, Cry1Ca, Cry1Cb, Cry1Da, Cry1Db,